

DATE: 02/11/2003

TIME: 13:40:15

PCT

PATENT APPLICATION: US/09/937,162 Ispar Set : A:\06501-085001.TXT Output Set: N:\CRF4\02112003\I937162.raw 4 <110 > APPLICANT: Sowa, Yoshihiro Orita, Metsuro 7 <1205 TITLE OF INVENTION: METHOD FOR SCREENING ANTICANCER AGENT 10 <100 FILE REFERENCE: 06501-085001 12 <140 - CURFENT APPLICATION NUMBER: US 09/937,162 C--> 13 <141> CURRENT FILING DATE: 2002-12-04 15 KINT FRICK APPLICATION NUMBER: PCT/US00/01778 16 <1:1 FRIER FILING DATE: 2006-03-23 18 KING FROOR APPLICATION NUMBER: JR 11-77350 ENTERED 19 -1111 - FELICE FILING DATE: 1999-03-23 01 406 - NUMBER OF SEQ ID NOS: 21 p? RITT - COFTWARE: FastSEQ for Windows Version 4.0 18 411. - Eag 10 80: 1 16 0111 LEMOTH: 16 of all a type: DMA. 18 Clb CR-AMISM: Artificial Sequence () O to LO EMATURE: 31 -0... - OTHER INFORMATION: primer BR (4) W - CERUENCE: 1 16 the organization of the state o 96 (L10 + SEQ 15 NO: 2 or the length: 1) 34 HOLL - CYEE: INA 1) Hill FREAMISM: Artificial Sequence 4% KOLO - FEATOFE: 4.2 -C. - (THEF INFORMATION: primer 44 H4 H FEGUENCE: 2 20 45 a mingagra coquestoctt 47 -111 - PEQ II NO: 3 in kuli - LEMGTH: 20 44 AUG - TYPE: INA 10 Miles OF GAMESM: Artificial Sequence ROGER - FEATURE: 33 MARY OTHER INFORMATION: primer Spatt SEQUENCE: 3 20 ,5 trisagoaq qogggacccq 38 and SEQ ID NO: 4 19 %21. [ENGIH: 14 60 821. 8 TYPE: DNA €1 + 21 + OFFAMISM: Artificial Sequence 63 J. BELATURE: 64 WILL OTHER INFORMATION: primer

RAW SEQUENCE LISTING

66 <4(U. SEQUENCE: 4

RAW SEQUENCE LISTING

FALENT AFFILINATION: US/09/937,162

DATE: 02/11/2003 TIME: 13:45:15

Input Ge: : A:\06501-085001.TXT

Output Set: N:\CRF4\02112003\I937162.raw

	1.4
67 बदबपुर्वाचुबपुरः ¹ 10व	. '1
69 32102 3EQ ID 10: 5	
76 <211 > LENGTH: 15	
71 KR12 - TYPE: DNA	
72 K.21: - ORSANISM: Artificial Sequence	
W ON THE PRAITIRE:	
75 &223: OTHER INFORMATION: primer	
7" (100. SEQUENCE: 5	7 ()
78 talaageda ttige	
80 (200 BEQ ID 10: 6	
81 <2.10 LENGTH: 10	
82 FALS TYPE: DNA	
83 CLUER ORGANISM: Artificial Sequence	
85 T. COMMERCE:	
86 - The OTHER INFORMATION: primer	
8:: 10:C: SEQUENCE: 6	30
th assistanta agugaaaggt aaccoggogg	. 2 4 7
91 =110	
92 (211) LHNGTH: 31	
9/ KIII. TYPE: ENA	
94 KM CORSANISM: Artificial Sequence	
9. FTATURF:</td <td></td>	
9 K.H. OTHER INFORMATION: primer	
9 · K: SEÇUENCE: 9	15
1 Classifications colors	# */
100 GOOD SEPOLE NO. 8	
10: A HE LENGTH: .3	
104 -0. LD: TYPE: DNA	
1 Por the CRUANISM: Artificial Sequence	
10% R.L. FEATURE:	
10to C. Ho OTHER INFORMATION: primer	
115 H45 F SELUENCE: 8	23
111 orrgaticat toplagtget get	20
11: <llo(- 1e="" 3e)="" 9<="" no:="" td=""><td></td></llo(->	
114 - CTIP LENGTH: +0	
110 C.H. TYFE: DNA	
116 4.18 + GREANISM: Artificial Sequence	
11+ KL: H FEATURE:	
1% + cm. + - OTHER INFORMATION: primer	
131 (40% SEQUENCE: 9	30
1.h. in Francist tachedattg totoatttoc	50
134 KMC+ SE2 II NO: 10	
1.35 K.111 K TENGTH: 1.16	
1 to Kill TYPE: ONA	
1.:: <: ORGANISM: Artificial Sequence	
12 + <2 - FEATURE:	
1:0 cl. s OTHER INFORMATION: primer	
182 <400 / SEQUENCE: 10	06
133 egggatecaa etetatagat tetget	26

RAW SEQUENCE LISTING

FATERET APPLICATION: US/09/937,162

DATE: 02/11/2000 TRME: 13:40:15

Imput det : A:\06501-085001.TXT Output Cet: N:\CRF4\02112003\1937162.raw

1 21	- Eig. dEg ID No: 11	
	WHO IENTE: 26	
	<212> TYPE: DNA	
	REINZ IICH. DAM REZICO GRGANISM: Artificial Sequence	
	K32Co FFATURE:	
	ACT A CTHIR UNPORMATION: primer	
	MOCO SEQUENCE: 11	26
	poquaticoca ctgtaactgt tigtag	20
	inter sec in Mo: 12	
	KALLY LENGTE: 28	
	HAND CHEANISM: Artificial Sequence	
	FRACURE:	
110	FILTER OFFER INFORMATION: primer	
1!;	HIGH SEQUENCE: 12	
1!	pountocog chetratean acottact	28
1	- 31 C- 315, 11 NO: 19	
	Allo dengie: 21	
	+ (. IYER: DNA	
	TERRIT TERMISM: Artificial Sequence	
	COLUMN BEATURE:	
	- NOTE OF HER INFORMATION: primer	
	-au EFTUEMCE: 13	
	: print.cog kartsatgod gaoggada	28
	31% 3F. II NO: 14	
	SERVICE LENGTH: SE	
	HATTAN TYPE: DNA	
	FULK CHUANISM: Artificial Sequence	
	A. P. FEARUFE:	
	- 1. 1. 17 HEF INFORMATION: primer	
	-4400 - SEAGENCE: 14	
	ermuteena qqqasattat atocagte	28
	-0.14	
	11 * I FASTE: 28	
	P. 1. TYPE: DNA	
	- 1	
	-1. The FRATURE:	
	-0.00 - OTHER INFORMATION: primer	
	(400 - SEQUENCE: 15	28
	rigiaticas gaitgatets aattigat	20
	-0.1 - FEQ ID NO: 16	
	HANTER LENGTH: PE	
	- ANTA - IVEE: DNA	
	COLORDANISM: Artificial Sequence	
	······································	
	- 12 - PTHER INFORMATION: primer	
	GATON - CHOURNER: 16	30
	ingratesty magneattyt otgagaad	28
2J1	<210 - SEQ ID NO: 17	

RAW SEQUENCE LISTING

FALENT APPLICATION: US/09/937,162 TIME: 12:40:15

DATE: 02/11/2003

Input Fot : A:\06501-085001.TXT

Output Set: N:\CRF4\02112003\I937162.raw

	1.1 %	• 2112 LENGTH: 28	
	203	<21z. TYPE: LNA	
		8:15 ORCANISM: Artificial Sequence	
	206	<pre><22(> FEATURE:</pre>	
	.:(7	<pre><eled< th=""><th></th></eled<></pre>	
	3.9	- And S. SEQUENCE: 17	
	()	cqqqatccaa qatctgaaga atgaacct	28
		-2'0> SEQ ID NO: 18	
	3	C. 11 > LENGTH: 28	
	: 1.4	COLO TYFE: ENA	
	Ē.	Hilly CRCANISM: Artificial Sequence	
	X .	FEATURE:	
		-222-5 CTHEE INFORMATION: primer	
		-CHOUGE SEQUENCE: 18	
		cytonecesa aggeeedage	28
		€11 0 CEQ 16 NO: 19	
		REGILE DENGTH: 17	
		INTERIOR	
		RELET CREAMISM: Artificial Sequence	
		CAR D FEATURE:	
		THE CATHER INFORMATION: exemplary motif	
		FRUENCE: 19	1.7
		, it gamag the con-	
		TOTAL SECTION 10	
		LIFT LENGTH: 16	
		ANTINO TY:E: INA	
		R. TRANCEMANISM: Artificial Sequence	
		State of the information: exemplary motif	
T.T \		<pre><221> NAME/KEY: misc_feature</pre>	
W>		ELLI LOCATION: (1)(16)	
		$+0.5 \times 0$ THEE INFORMATION: $n = A, T, C \text{ or } G$	
W>		<400> 20	
		ctgtnnnnn nnacag	16
., ,		-1.15 - SEQ IP NO: 21	
	35.1	CD11 - DENGCH: 19	
		ROLLING TYPE: DNA	
		Hally + ORGANISM: Artificial Sequence	
		FILTER FEATURE:	
	15,5	HILLS - OTHER INFORMATION: exemplary motif	
		(40) > SEQUENCE: 21	
	21.8	topptatoag tgatagaga	19

RAW SEQUENCE LISTING ERROR SUMMARY WALL: 4-2/11/2001; MARKET AND HAVATION: US/09/937,162

FIME: 13:44:16

Input Set : A:\06501-085001.TXT

Output Det: N:\CRF4\02112003\I937162.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:20; N Fos. 5,6,7,8,9,10,11,12